#### Lab FAT

**Machine learning** 

**Logistic regression** 

Link to dataset: [https://archive.ics.uci.edu/ml/datasets/Cervical+cancer+%28Risk+Factors%29]

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## Importing the dependancies

```
In [73]:
```

```
import pandas as pd
import numpy as np
import seaborn as sns # plotting
#eval metric
from sklearn.metrics import f1_score
from sklearn.metrics import roc_auc_score
from yellowbrick.classifier import ROCAUC
#model
from sklearn.linear_model import LogisticRegressionCV

#splitting train and test
from sklearn.model_selection import train_test_split
```

## **Understanding the dataset**

```
(int) Age
(int) Number of sexual partners
(int) First sexual intercourse (age)
(int) Num of pregnancies
(bool) Smokes
(bool) Smokes (years)
(bool) Smokes (packs/year)
(bool) Hormonal Contraceptives
(int) Hormonal Contraceptives (years)
(bool) IUD
(int) IUD (years)
(bool) STDs
(int) STDs (number)
(bool) STDs:condylomatosis
(bool) STDs:cervical condylomatosis
(bool) STDs:vaginal condylomatosis
(bool) STDs:vulvo-perineal condylomatosis
(bool) STDs:syphilis
(bool) STDs:pelvic inflammatory disease
(bool) STDs:genital herpes
(bool) STDs:molluscum contagiosum
(bool) STDs:AIDS
(bool) STDs:HIV
(bool) STDs:Hepatitis B
(bool) STDs:HPV
(int) STDs: Number of diagnosis
(int) STDs: Time since first diagnosis
(int) STDs: Time since last diagnosis
(bool) Dx:Cancer
(bool) Dx:CIN
```

(bool) Dx:HPV

(bool) Dx (bool) Hinselmann: target variable (bool) Schiller: target variable (bool) Cytology: target variable (bool) Biopsy: target variable

## Reading the dataframe

In [ ]:

Out[]:

```
df = pd.read_csv('/content/risk_factors_cervical_cancer.csv')
In []:
# displaying the first 5 rows of the dataset
df.head()
Out[]:
```

	Age	Number of sexual partners	First sexual intercourse	Num of pregnancies	Smokes	Smokes (years)	Smokes (packs/year)	Hormonal Contraceptives	Hormonal Contraceptives (years)	IUD	IUD (years)	STE
0	18	4.0	15.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0
1	15	1.0	14.0	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0
2	34	1.0	?	1.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0
3	52	5.0	16.0	4.0	1.0	37.0	37.0	1.0	3.0	0.0	0.0	0
4	46	3.0	21.0	4.0	0.0	0.0	0.0	1.0	15.0	0.0	0.0	0
4												·

```
In []:

print("Number of rows = ", df.shape[0])
print("Number of columns = ", df.shape[1])

Number of rows = 858
Number of columns = 36
```

## **Basic statistical description**

```
In []:
df.describe()
```

```
STDs:
             Age
                    Number of
                                Dx:Cancer
                                                Dx:CIN
                                                            Dx:HPV
                                                                             Dx Hinselmann
                                                                                                  Schiller
                                                                                                              Citology
                                                                                                                           Bior
                     diagnosis
count 858.000000
                                                                                  858.000000 858.000000 858.000000
                   858.000000
                               858.000000
                                            858.000000 858.000000
                                                                     858.000000
                                                                                                                       858.0000
        26.820513
                     0.087413
                                  0.020979
                                              0.010490
                                                           0.020979
                                                                       0.027972
                                                                                    0.040793
                                                                                                 0.086247
                                                                                                             0.051282
                                                                                                                          0.064^{\circ}
mean
         8.497948
  std
                     0.302545
                                  0.143398
                                              0.101939
                                                           0.143398
                                                                       0.164989
                                                                                    0.197925
                                                                                                 0.280892
                                                                                                             0.220701
                                                                                                                          0.2450
 min
        13.000000
                     0.000000
                                  0.000000
                                              0.000000
                                                           0.000000
                                                                       0.000000
                                                                                    0.000000
                                                                                                 0.000000
                                                                                                             0.000000
                                                                                                                          0.0000
 25%
        20.000000
                     0.000000
                                  0.000000
                                              0.000000
                                                           0.000000
                                                                       0.000000
                                                                                    0.000000
                                                                                                 0.000000
                                                                                                             0.000000
                                                                                                                          0.0000
        25.000000
                     0.000000
                                  0.000000
                                              0.000000
                                                           0.000000
                                                                       0.000000
                                                                                    0.000000
                                                                                                 0.000000
                                                                                                             0.000000
                                                                                                                          0.0000
 50%
        32.000000
                     0.000000
                                  0.000000
                                              0.000000
                                                           0.000000
                                                                       0.000000
                                                                                    0.000000
                                                                                                 0.000000
                                                                                                             0.000000
                                                                                                                          0.0000
 75%
        84.000000
                     3.000000
                                  1.000000
                                              1.000000
                                                           1.000000
                                                                       1.000000
                                                                                                             1.000000
                                                                                                                          1.0000
                                                                                    1.000000
                                                                                                 1.000000
 max
```

1

#### ₩ Þ

### In [ ]:

### df.dtypes

### Out[]:

Age	int64
Number of sexual partners	object
First sexual intercourse	object
Num of pregnancies	object
Smokes	object
Smokes (years)	object
Smokes (packs/year)	object
Hormonal Contraceptives	object
Hormonal Contraceptives (years)	object
IUD	object
IUD (years)	object
STDs	object
STDs (number)	object
STDs:condylomatosis	object
STDs:cervical condylomatosis	object
STDs:vaginal condylomatosis	object
STDs:vulvo-perineal condylomatosis	object
STDs:syphilis	object
STDs:pelvic inflammatory disease	object
STDs:genital herpes	object
STDs:molluscum contagiosum	object
STDs:AIDS	object
STDs:HIV	object
STDs:Hepatitis B	object
STDs: HPV	object
STDs: Number of diagnosis	int64
STDs: Time since first diagnosis	object
STDs: Time since last diagnosis	object
Dx:Cancer	int64
Dx:CIN	int64
Dx: HPV	int64
Dx	int64
Hinselmann	int64
Schiller	int64
Citology	int64
Biopsy	int64
dtype: object	

#### In [ ]:

### df.isnull().sum()

### Out[]:

Age

Number of sexual partners	0				
First sexual intercourse	0				
Num of pregnancies	0				
Smokes	0				
Smokes (years)	0				
Smokes (packs/year)	0				
Hormonal Contraceptives	0				
Hormonal Contraceptives (years)	0				
IUD	0				
IUD (years)	0				
STDs	0				
STDs (number)	0				
STDs:condylomatosis					
STDs:cervical condylomatosis					
STDs:vaginal condylomatosis	0				
STDs:vulvo-perineal condylomatosis	0				
STDs:syphilis	0				
STDs:pelvic inflammatory disease	0				
STDs:genital herpes	0				
STDs:molluscum contagiosum	0				
	-				

0

```
STDs:AIDS
                                       0
                                       0
STDs:HIV
                                       0
STDs: Hepatitis B
                                       0
STDs:HPV
STDs: Number of diagnosis
                                       0
STDs: Time since first diagnosis
                                       0
STDs: Time since last diagnosis
                                       0
Dx:Cancer
                                       0
Dx:CIN
Dx: HPV
                                       0
Dχ
                                       0
                                       0
Hinselmann
                                       0
Schiller
                                       0
Citology
                                       0
Biopsy
dtype: int64
In [ ]:
for col in np.array(df.columns()):
  print(col)
                                           Traceback (most recent call last)
<ipython-input-24-69a1d7b68ac4> in <module>()
---> 1 for col in np.array(df.columns()):
      2 print(col)
TypeError: 'Index' object is not callable
In [ ]:
for col in np.array(df.columns):
  df.loc[df[col] == '?', col] = np.NaN
In [ ]:
df.isnull().sum()
Out[]:
                                         0
Age
Number of sexual partners
                                        26
                                         7
First sexual intercourse
                                        56
Num of pregnancies
                                        13
Smokes
                                        13
Smokes (years)
Smokes (packs/year)
                                        13
Hormonal Contraceptives
                                       108
Hormonal Contraceptives (years)
                                       108
IUD
                                       117
IUD (years)
                                       117
STDs
                                       105
                                       105
STDs (number)
STDs:condylomatosis
                                       105
                                       105
STDs:cervical condylomatosis
STDs:vaginal condylomatosis
                                       105
STDs:vulvo-perineal condylomatosis
                                       105
                                       105
STDs:syphilis
STDs:pelvic inflammatory disease
                                       105
STDs:genital herpes
                                       105
STDs:molluscum contagiosum
                                       105
STDs:AIDS
                                       105
STDs:HIV
                                       105
STDs: Hepatitis B
                                       105
STDs:HPV
                                       105
STDs: Number of diagnosis
                                         0
STDs: Time since first diagnosis
                                       787
STDs: Time since last diagnosis
                                       787
Dx:Cancer
                                         0
Dx:CIN
                                         0
Dx:HPV
                                         0
```

```
DXUHinselmann0Schiller0Citology0Biopsy0dtype: int64
```

```
Fixing missing values and datatypes
In [59]:
df = df.fillna(0)
In [69]:
for id, dt in enumerate(np.array(df.dtypes)):
  if dt=='0':
    if np.array(df[df.columns[id]].value counts()).shape[0] == 2:
      df[df.columns[id]] = df[df.columns[id]].astype("float")
      df[df.columns[id]] = df[df.columns[id]].astype("int")
      df[df.columns[id]] = df[df.columns[id]].astype("float")
      df[df.columns[id]] = df[df.columns[id]].astype("int")
In [70]:
df.dtypes
Out[70]:
                                       float64
Number of sexual partners
                                      float64
First sexual intercourse
                                        int64
Num of pregnancies
                                        int64
Smokes
                                        int64
Smokes (years)
                                        int64
                                        int64
Smokes (packs/year)
                                        int64
Hormonal Contraceptives
Hormonal Contraceptives (years)
                                        int64
IUD
                                        int64
IUD (years)
                                        int64
STDs
                                        int64
STDs (number)
                                        int64
STDs:condylomatosis
                                        int64
STDs:cervical condylomatosis
                                      float64
STDs:vaginal condylomatosis
                                        int64
STDs:vulvo-perineal condylomatosis
                                        int64
                                        int64
STDs:syphilis
STDs:pelvic inflammatory disease
                                        int64
STDs:genital herpes
                                        int64
STDs:molluscum contagiosum
                                        int64
STDs:AIDS
                                      float64
                                        int64
STDs:HIV
STDs:Hepatitis B
                                        int64
STDs:HPV
                                        int64
STDs: Number of diagnosis
                                      float64
STDs: Time since first diagnosis
                                        int64
STDs: Time since last diagnosis
                                        int64
                                      float64
Dx:Cancer
Dx:CIN
                                      float64
Dx: HPV
                                      float64
                                      float64
Hinselmann
                                      float64
Schiller
                                      float64
```

float64

float64

In [71]:

Citology

dtype: object

Biopsy

Some of the rows have no values 1 like row 1 and 2 this might be an issue for softmax predictions while using MLP

```
In [74]:
```

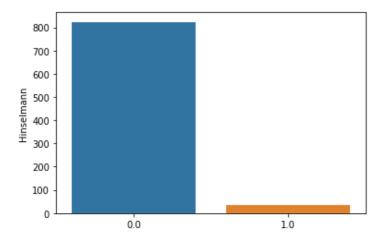
```
sns.barplot(df['Hinselmann'].value_counts().index, df['Hinselmann'].value_counts())
```

/usr/local/lib/python3.7/dist-packages/seaborn/\_decorators.py:43: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional a rgument will be `data`, and passing other arguments without an explicit keyword will result in an error or misinterpretation.

FutureWarning

#### Out[74]:

<matplotlib.axes.\_subplots.AxesSubplot at 0x7f900b243150>



# **Train test split**

```
In [79]:
```

```
from sklearn.model_selection import train_test_split
X = df.iloc[:, :-4]
y = df['Hinselmann']
# using stratified to ensure equal 1's in the test set
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.33, random_state=4
2, stratify=y)
```

#### In [80]:

```
from sklearn.linear_model import LogisticRegressionCV
lr = LogisticRegressionCV(cv=5, random_state=0).fit(X_train, y_train)

/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:940: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
    extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG)
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/ logistic.py:940: Convergence
```

```
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
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  extra warning msg= LOGISTIC SOLVER CONVERGENCE MSG)
/usr/local/lib/python3.7/dist-packages/sklearn/linear model/ logistic.py:940: Convergence
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STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
Increase the number of iterations (max iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
  extra warning msg= LOGISTIC SOLVER CONVERGENCE MSG)
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:940: Convergence
Warning: lbfgs failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
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/usr/local/lib/python3.7/dist-packages/sklearn/linear model/ logistic.py:940: Convergence
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    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG)
/usr/local/lib/python3.7/dist-packages/sklearn/linear model/ logistic.py:940: Convergence
```

```
Warning: lbfgs failed to converge (status=1):
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/usr/local/lib/python3.7/dist-packages/sklearn/linear model/ logistic.py:940: Convergence
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  extra warning msg= LOGISTIC SOLVER CONVERGENCE MSG)
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:940: Convergence
Warning: lbfgs failed to converge (status=1):
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   https://scikit-learn.org/stable/modules/preprocessing.html
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   https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
  extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG)
/usr/local/lib/python3.7/dist-packages/sklearn/linear_model/_logistic.py:940: Convergence
Warning: lbfgs failed to converge (status=1):
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   https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
   https://scikit-learn.org/stable/modules/linear model.html#logistic-regression
 extra warning msg= LOGISTIC SOLVER CONVERGENCE MSG)
In [82]:
```

```
lr = LogisticRegressionCV(cv=5, random_state=0, max_iter=1000).fit(X_train, y_train)
```

## **Evaluation metrics on test set**

Out[90]:

```
In [89]:

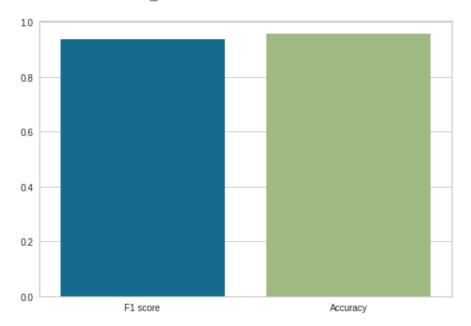
print("F1 Score = ", f1_score(y_test, lr.predict(X_test), average='weighted'))
print("Accuracy = ", lr.score(X_test, y_test))

F1 Score = 0.9370756915594285
Accuracy = 0.9577464788732394

In [90]:

sns.barplot(['F1 score', 'Accuracy'], [0.9370756915594285, 0.9577464788732394])

/usr/local/lib/python3.7/dist-packages/seaborn/_decorators.py:43: FutureWarning: Pass the following variables as keyword args: x, y. From version 0.12, the only valid positional a rgument will be 'data', and passing other arguments without an explicit keyword will result in an error or misinterpretation.
   FutureWarning
```

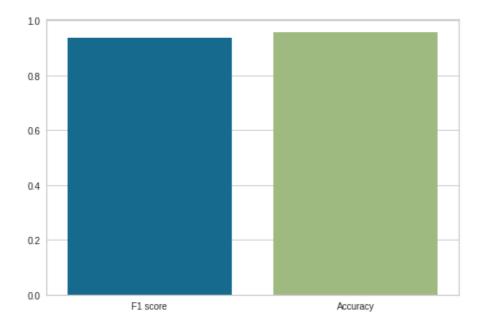


#### In [94]:

```
import warnings
warnings.simplefilter("ignore")
import matplotlib.pyplot as plt
for col in ['Hinselmann', 'Schiller', 'Citology', 'Biopsy']:
 X = df.iloc[:, :-4]
 y = df[col]
 print(col)
  # using stratified to ensure equal 1's in the test set
 X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.33, random_state
=42, stratify=y)
 lr = LogisticRegressionCV(cv=5, random_state=0, max_iter=1000).fit(X_train, y_train)
 print("F1 Score = ", f1_score(y_test, lr.predict(X_test), average='weighted'))
 print("Accuracy = ", lr.score(X_test, y_test))
 sns.barplot(['F1 score', 'Accuracy'], [f1_score(y_test, lr.predict(X_test), average='w
eighted'), lr.score(X test, y test)])
  plt.show()
```

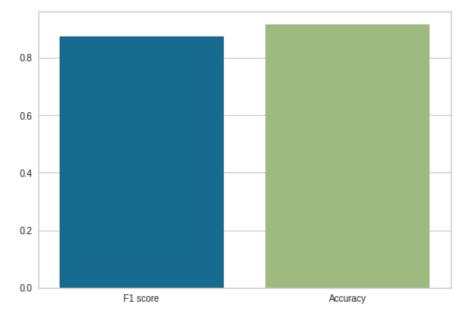
# Hinselmann F1 Score = 0.9370

F1 Score = 0.9370756915594285Accuracy = 0.9577464788732394



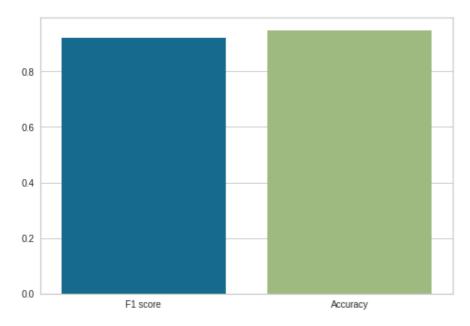
#### Schiller

F1 Score = 0.8751035625517812 Accuracy = 0.9154929577464789



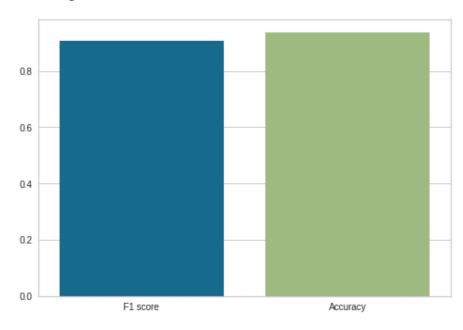
Citology

F1 Score = 0.9214909711433155 Accuracy = 0.9471830985915493



Biopsy

F1 Score = 0.9059667093469911 Accuracy = 0.9366197183098591



In [98]:

from allocus model colockies import Cuidecouches

In [ ]: